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USPT,EPAB,DWPI	muta\$8 near10 (recombin\$5 adj3 site\$1)	344	<u>L6</u>
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USPT,EPAB,DWPI	11 not lox	690	<u>L4</u>
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USPT,EPAB,DWPI	11 near10 att	5	<u>L2</u>
USPT,EPAB,DWPI	muta\$8 near10 (recombin\$5 near5 site\$1)	742	<u>L1</u>

L10 ANSWER 2 OF 3 CAPLUS COPYRI 2001 ACS  
AN 1987:97068 CAPLUS  
DN 106:97068  
TI Mutational analysis of integrase arm-type binding sites of bacteriophage  
lambda. Integration and excision involve distinct interactions of  
integrase with arm-type sites  
AU Bauer, Carl E.; Hesse, Steven D.; Gumpert, Richard I.; Gardner, Jeffrey F.  
CS Dep. Microbiol., Univ. Illinois, Urbana, IL, 61801, USA  
SO J. Mol. Biol. (1986), 192(3), 513-27  
CODEN: JMOBAK; ISSN: 0022-2836  
DT Journal  
LA English  
AB Integrative recombination between specific attachment (att) regions of the  
bacteriophage lambda genome (attP) and the Escherichia coli genome (attB)  
results in a prophage flanked by the hybrid recombinant sites attL and  
attR. Each att site contains sequences to which proteins involved in  
recombination bind. Using site-directed mutagenesis, a related set of  
point mutations was constructed within each of the five Int arm-type  
binding sites located within attP, attL and attR. Footprint analyses of  
binding demonstrate that mutating the arm-type sites significantly  
disrupts the binding of Int. **Recombination** analyses of  
**mutant att** sites in vivo and in vitro demonstrate that  
only three wild-type arm-type sites within attP are required for efficient  
integrative recombination. Similar analyses demonstrate that efficient  
excision can occur with two other different sets of wild-type arm-type  
sites in attL and attR. Integrative and excisive recombination may  
involve interactions of Int with distinct and different subsets of  
arm-type sites.

AN 1997:504771 CAPLUS

DN 127:215643

TI Molecular engineering with the FRT sequence of the yeast 2.mu.m plasmid:  
[cir.degree.] segregant enrichment by counterselection for 2.mu.m  
site-specific recombination

AU Storici, Francesca; Bruschi, Carlo V.

CS Microbiology Group, ICGEB, AREA Science Park, Padriciano 99, I-34012,  
Trieste, Italy

SO Gene (1997), 195(2), 245-255 *shulq7*  
CODEN: GENED6; ISSN: 0378-1119

PB Elsevier

DT Journal

LA English

IT 195130-43-9

RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological  
study); USES (Uses)

(BglII site-contg. **mutant FRT** sequence; mol.

engineering with FRT sequence of yeast 2.mu.m plasmid: [cir.degree.]

segregant enrichment by counterselection for 2.mu.m site-specific  
recombination)

IT 195130-42-8

RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological  
study); USES (Uses)

(XhoI site-contg. **mutant FRT** sequence; mol.

engineering with FRT sequence of yeast 2.mu.m plasmid: [cir.degree.]

segregant enrichment by counterselection for 2.mu.m site-specific  
recombination)

OK

AN 1994:647354 CAPLUS

DN 121:247354

TI Use of Mutated FLP Recognition Target (FRT) Sites for the Exchange of Expression Cassettes at Defined Chromosomal Loci

AU Schlake, Thomas; Bode, Juergen

CS Gesellschaft fuer Biotechnologische Forschung mbH, Braunschweig-Stoeckheim, D-38124, Germany

SO Biochemistry (1994), 33(43), 12746-51

CODEN: BICHAW; ISSN: 0006-2960

DT Journal

LA English

AB Using the FLP/FRT system for site-specific recombination and the wild-type recognition site (FRT) in conjunction with certain **mutant FRT** sites, it becomes possible to provoke, with high yield, a double-reciprocal crossover event in cultured mammalian cells. It is demonstrated that this technol. enables a targeting of expression cassettes to appropriate chromosomal ref. sites in the recipient cell to improve the concepts of reverse genetics. The design of **mutant FRT** sites promoting such a process will be delineated. Our results show that the five spacer mutations tested are functional as the wild-type but differ in the extent of their cross-recombination, which has to be minimized for their simultaneous usage.

IT Mammal

(FLP/FRT system for site-specific recombination and the wild-type recognition site (FRT) with certain **mutant FRT** sites cause, with high yield, a double-reciprocal crossover event in cultured mammalian cells)

IT Recombination, genetic

(double-reciprocal; FLP/FRT system for site-specific recombination and the wild-type recognition site (FRT) with certain **mutant FRT** sites cause, with high yield, a double-reciprocal crossover event in cultured mammalian cells)

IT Recombination, genetic

(site-specific, FLP/FRT system for site-specific recombination and the wild-type recognition site (FRT) with certain **mutant FRT** sites cause, with high yield, a double-reciprocal crossover event in cultured mammalian cells)

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Q4501.052

AN 1982:434047 CAPLUS

DN 97:34047

TI Biochemical analysis of att-defective mutants of the phage lambda site-specific recombination system

AU Ross, Wilma; Shulman, Marc; Landy, Arthur

CS Div. Biol. Med., Brown Univ., Providence, RI, 02912, USA

SO J. Mol. Biol. (1982), 156(3), 505-29

CODEN: JMOBAK; ISSN: 0022-2836

DT Journal

LA English

ST phage lambda **att mutant** sequence; DNA sequence lambda **att mutant**; recombination site specific lambda att; protein gene int binding lambda

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AN 1971:136879 CAPLUS

DN 74:136879

TI Deletion mutants of bacteriophage lambda. II. Genetic properties of att-defective mutants

AU Parkinson, John S.

CS Div. Biol., California Inst. Technol., Pasadena, Calif., USA

SO J. Mol. Biol. (1971), 56(2), 385-401

CODEN: JMOBAK

DT Journal

LA English

AB Viable, integration-defective deletion mutants of phage .lambda. were examd. with the technique of Int-promoted recombination between phages. The types of mutants found and their properties are consistent with a 3-component model of att.phi.. The results show that att.phi. contains a unique locus for integration cross-overs which is bordered on each side by recognition sequences essential for normal integration. The role of these recognition sequences in integration was studied by analyzing the pattern of Int-promoted recombination between phage contg. various types of **mutant att** sites. It was found that the integration system of .lambda. can function with a variety of defective att sites; however, no simple pattern could be deduced from these results. Evidently, the .lambda. integration system is considerably more complex than was at first believed, and very unlike systems of generalized recombination.

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